CLAIMS

1. A sample analyzing method, which comprises:

a step (a) of correcting at least a one-dimensional parameter in multi-dimensional data obtained as a result of the analysis of a sample; and

a step (b) of comparing the corrected data obtained in said step (a) for multiple samples.

2. The sample analyzing method according to claim 1, wherein said multi-dimensional data is three-dimensional data consisting of a parameter indicating a mass-to-charge ratio, a parameter indicating ionic intensity, and a parameter indicating a retention time, obtained as a result of chromatography mass spectrometry, and wherein the parameter indicating a retention time is corrected in said step (a).

3. The sample analyzing method according to claim 1, wherein, in said step (a), profiles regarding parameters, from which a parameter as a correction target has been excluded, are used as reference profiles, and wherein using an evaluation function acting as a scale of position similarity regarding a plurality of reference profiles among multiple samples, the position of each profile is determined as a problem of finding an optimum solution which optimizes the value of said evaluation function.

4. The sample analyzing method according to claim 3, wherein said evaluation function is defined with one or more terms selected from the group consisting of the following terms (1) to (5):

(1) a term regarding similarity and/or distance among profiles regarding a parameter of a correction target;

(2) a term regarding similarity and/or distance among profiles regarding a reference profile;

(3) a term regarding the degree of concordance of data points among profiles as comparison targets;

(4) a term regarding the degree of discordance of data points among profiles as comparison targets;

(5) a term regarding the degree of concordance or discordance of reference material-derived signals among profiles as comparison targets; and

(6) a term regarding the degree of concordance in the previous comparison during repeated comparison operations.

5. The sample analyzing method according to claim 3, wherein, in said step (a), dynamic programming algorithm is used, when the value of said evaluation function is optimized as a problem of finding an optimum solution regarding said parameter of a correction target.

6. The sample analyzing method according to claim 5, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, the score of a correspondence regarding data points derived from a reference material is set by a point-addition scoring system.

7. The sample analyzing method according to claim 5, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, a constraint condition is set, in which a correspondence regarding data points derived from a reference material is necessarily corresponded at a designated point.

8. The sample analyzing method according to claim 1, wherein said sample comprises a protein group and/or a peptide group.

9. The sample analyzing method according to claim 1, wherein said multiple samples comprise a reference material.

10. The sample analyzing method according to claim 9, wherein said reference material is at least one type of peptide selected from the group consisting of peptide T (Ala-Ser-Thr-Thr-Asn-Tyr-Thr), β-casomorphin-7 (Tyr-Pro-Phe-Pro-Gly-Pro-Ile), and a structural analog thereof.

11. The sample analyzing method according to claim 9, wherein said reference material is added to said sample in a state where it is immobilized in gel.

12. A sample analyzing program for allowing a computer to execute:

a procedure (a) of inputting multi-dimensional data obtained as a result of the analysis of a sample;

a procedure (b) of correcting the data of at least a one-dimensional parameter from among the inputted multi-dimensional data; and

a procedure (c) of comparing multi-dimensional data including the data corrected in said procedure (b) for multiple samples.

13. The sample analyzing program according to claim 12, wherein said multi-dimensional data is three-dimensional data consisting of a parameter indicating a mass-to-charge ratio, a parameter indicating ionic intensity, and a parameter indicating a retention time, obtained as a result of chromatography mass spectrometry, and wherein the parameter indicating a retention time is corrected in said procedure (b).

14. The sample analyzing program according to claim 12, wherein, in said procedure (b), profiles regarding parameters, from which a parameter as a correction target has been excluded, are used as reference profiles, and wherein using an evaluation function acting as a scale of position similarity regarding a plurality of reference profiles among multiple samples, the position of each profile is determined by optimizing the value of said evaluation function as a problem of finding an optimum solution.

15. The sample analyzing program according to claim 14, wherein said evaluation function is defined with one or more terms selected from the group consisting of the following terms (1) to (5):

(1) a term regarding similarity and/or distance among profiles regarding a parameter of a correction target;

(2) a term regarding similarity and/or distance among profiles regarding a reference profile;

(3) a term regarding the degree of concordance of data points among profiles as comparison targets;

(4) a term regarding the degree of discordance of data points among profiles as comparison targets;

(5) a term regarding the degree of concordance or discordance of reference material-derived signals among profiles as comparison targets; and

(6) a term regarding the degree of concordance in the previous comparison during repeated comparison operations.

16. The sample analyzing program according to claim 14, wherein, in said procedure (a), dynamic programming algorithm is used, when the value of said evaluation function is optimized as a problem of finding an optimum solution regarding said parameter of a correction target.

17. The sample analyzing program according to claim 16, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, the score of a correspondence regarding data points derived from a reference material is set by a point-addition scoring system.

18. The sample analyzing program according to claim 16, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, a constraint condition is set, in which a correspondence regarding data points derived from a reference material is necessarily corresponded at a designated point.

19. The sample analyzing program according to claim 12, wherein said sample comprises a protein group and/or a peptide group, and wherein multi-dimensional data derived from said protein group and/or peptide group are analyzed.

20. The sample analyzing program according to claim 12, wherein said multiple samples comprise reference materials, and wherein multi-dimensional data derived from these reference materials and multi-dimensional data derived from components contained in said samples are used in said procedure (b).

21. The sample analyzing program according to claim 20, wherein said reference material is at least one type of peptide selected from the group consisting of peptide T (Ala-Ser-Thr-Thr-Asn-Tyr-Thr), β-casomorphin-7 (Tyr-Pro-Phe-Pro-Gly-Pro-Ile), and a structural analog thereof.

22. The sample analyzing program according to claim 20, wherein said reference material is added to said sample in a state where it is immobilized in gel.